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### IN THE CLAIMS

The claims as currently presented and under consideration, are presented below.

1-10 (Cancelled)

11. (Currently amended): A modified xylanase comprising a polypeptide having an amino acid sequence as set forth in SEQ ID NO:1, wherein the sequence has at least one substituted amino acid residue at a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence.

12. (Currently amended): The xylanase according to Claim 11, wherein the at least one substitution is at residue 144 ~~selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.~~

13. (Currently amended): The xylanase according to Claim 12, wherein the ~~modified xylanase has at least one substitution is selected from the group consisting of: H22K, S65C, N92C, F93W, N97R, V108H, H144C, or H144K, F180Q and S186C.~~

14. (Currently amended): The xylanase according to Claim 13, wherein the xylanase has at least a second substitution selected from the group consisting of: the following mutations: H22K, S65C, N92C, V108H, H144G, F93W, N97R and H144K, S185C.

15. (Original): The xylanase according to Claim 13, wherein the xylanase has the following mutations: H144C and N92C.

16. (Original): The xylanase according to Claim 13, wherein the xylanase has the following mutations: F180Q, H144C and N92C.

17-19 (Cancelled)

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20. (Original): The xylanase according to Claim 13, wherein the xylanase has the following mutations: H22K, F180Q, H144C and N92C.

21. (Currently amended): A modified enzyme, the modified enzyme comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence.

22. (Currently amended): The enzyme according to Claim 21, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20% 90% in conserved regions common to at least 75% of family 11 xylanases.

23. (Original): The enzyme according to Claim 22, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

24. (Currently amended): A glycosyl hydrolase of Clan C comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence.

25. (Currently amended): The glycosyl hydrolase according to Claim 24, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20% 90% in conserved regions common to at least 75% of family 11 xylanases.

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26. (Original): The glycosyl hydrolase according to Claim 25, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

27. (Currently amended): A modified family 11 xylanase comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having a substituted amino acid residue at a position equivalent to 144 in SEQ ID NO: 1, wherein the position of the substituted amino acid is numbered from the amino acid after the signal and pro sequence ~~at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 18, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 168, 180, 184, 186, 188, 190 and +191.~~

28. (Currently amended): The xylanase according to Claim 27, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20% 90% in conserved regions common to at least 75% of family 11 xylanases.

29. (Currently amended): The xylanase according to Claim 28, wherein the amino acid sequence has at least one further substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

30-32 (Cancelled)

33. (Previously presented): The xylanase according to Claim 12, wherein the modified xylanase comprises a substitution at position 2, 28, 58, 144 and +191.

34. (Previously presented): The xylanase according to Claim 33, further comprising a substitution at a position selected from position 22, 65, 92, 93, 97, 108, 180, and 186.

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35. (Currently amended): The modified family 11 xylanase according to Claim 27, wherein the sequence homologous to the sequence set forth in SEQ ID NO:1 has at least ~~80%-97%~~ sequence identity to SEQ ID NO:1 in conserved regions common to at least 75% of family 11 xylanases.

36. (Previously presented): The xylanase according to Claim 35, wherein the modified xylanase has a substitution at positions 2, 28, 58, 144 and +191.

37. (Previously presented): The xylanase according to Claim 36, wherein the substitution at position 144 is K or C.

38-39 (Cancelled)

40. (New) The xylanase of claim 12, further comprising a second substitution at a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

41. (New) The xylanase of claim 27, further comprising at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10, 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

42. (New) The xylanase of claim 12 wherein the xylanase is obtained from *Trichoderma reesei*.